

1652

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SEP 26 2002

TECH CENTER 1600/2900



#19

1600

RAW SEQUENCE LISTING

DATE: 09/19/2002

PATENT APPLICATION: US/09/656,640A

TIME: 17:28:29

Input Set : A:\GC584-2-SEQLIST.TXT

Output Set: N:\CRF3\09192002\I656640A.raw

P.6

ENTERED

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4 <110> APPLICANT: Wang, Huaming
5      van Gastel, Frans
6      Aehle, Wolfgang
7      Rodrigues, Ana
8      Topozada, Amr
10 <120> TITLE OF INVENTION: Phenol Oxidizing Enzyme Variants
13 <130> FILE REFERENCE: GC584-2
15 <140> CURRENT APPLICATION NUMBER: US 09/656,640A
16 <141> CURRENT FILING DATE: 2000-09-07
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1958
24 <212> TYPE: DNA
25 <213> ORGANISM: Stachybotrys chartarum
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29 ggcggcagct ctgtcgatgc cagatccgtt gctggtcgat cgacagacat gccttccggt      120
30 ctccaagaaga ggcagacgca gctgagtcct cccctggcct tgtacgaagt gcctctgccg      180
31 atccctcctc tgaaggcgcc caagtagtaa gtacattcta taggctagca gagccaacgt      240
32 tgctaatacat tgcagtaccg tccccaaccc caacactgga gaggacatct tgtactacga      300
33 gatggagatt aggcccttct cccaccagat ctaccctgat ctggagccgg ccaacatggt      360
34 tggatacgaat ggcattgtccc caggacctac catcatcggt cctcgtggca ctgagagtgt      420
35 tgtccgcttc gtgaacagcg gagagaacac ctctcccaac agcgtccact tgcacggctc      480
36 tttctctcga gctccctttg atggttgggc tgaggacact acccagcctg gcgagtacaa      540
37 ggattactac taccccaaca ggcaggctgc ccgcatgctt tggtaaccatg accatgccat      600
38 gtccatcacc gccgagaacg cctacatggg tcaggctggt gtctacatga tccaggaccc      660
39 ggctgaggat gccctgaacc tccccagcgg ctacggcgag tttgatatacc ccttggttct      720
40 gactgccaaag cgatacaacg cagacggcac tctcttctcc accaatggag aggtttccag      780
41 cttctggggg gacgttattc aagtggtaag ttgagcccat tgagatgctt cagatcctag      840
42 aagtatcgat gtatgaaatt gtgcatgctc taaccagtgc tatcacagaa cggtcagcct      900
43 tggcctatgc tcaacgtgca gccgcgcaag taccgcttcc gcttcctcaa cgctgccgtc      960
44 tcacgctctt tcgctctgta tcttgctacc tctgaggatt cagagaccag acttcccttc      1020
45 caggctcattg ccgctgacgg tggctgtgctt gagggccctg ttgacactga cactctgtac      1080
46 atctctatgg ccgagcgtg ggaggttggt atcgacttct ccaccttcgc tggccagtcc      1140
47 atcgatatcc gcaaccttcc tgggtgctgac ggtctcggtg ttgagcctga gtttgataac      1200
48 actgacaagg tcatgcgatt cgtcgttgat gaagtccctg agtcgcccga cacttctgag      1260
49 gtgcctgcca acctccgaga tgttcccttc cccgaggcgg gcaactggga ccccgcaaac      1320
50 cccactgatg acgagacttt caccctcgcc cgtgctaatt gacagtggac aatcaacgga      1380
51 gttaccttct cggatgtcga gaaccgtctg ctccgcaatg tgccccgcga cactgttgag      1440
52 atctggcgac ttgagaacaa ctccaacggt tggactcacc ctggtcacat tcacctggtt      1500
53 gacttccgag tcctttctcg ttccactgcc cgtggagtcg agccttatga ggctgtggt      1560
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55 cctttcccggt aagttctcgc cttttaccta actgggttttc actcatgcta acatctacaa 1680
56 gtggtgtcta catgttgac tgccacaacc tgatccacga ggaccacgac atgatggctg 1740
57 ctttcaatgt cactgttctc ggtgactatg gctacaacta caccgagttc attgacccca 1800
58 tggagcctct ctggaggccc cgccccttcc tcctcggaga gttcgagaat ggctcgggtg 1860
59 acttcagcga gcttgccatc actgaccgca ttcaggagat ggctagcttc aaccctacg 1920
60 cccaggetga tgatgatgcc gctgaggagt agaccggt 1958
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63 <211> LENGTH: 583
64 <212> TYPE: PRT
65 <213> ORGANISM: Stachybotrys chartarum
67 <400> SEQUENCE: 2
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70 Gly Gly Ser Ser Val Asp Ala Arg Ser Val Ala Gly Arg Ser Thr Asp
71 20 25 30
72 Met Pro Ser Gly Leu Thr Lys Arg Gln Thr Gln Leu Ser Pro Pro Leu
73 35 40 45
74 Ala Leu Tyr Glu Val Pro Leu Pro Ile Pro Pro Leu Lys Ala Pro Asn
75 50 55 60
76 Thr Val Pro Asn Pro Asn Thr Gly Glu Asp Ile Leu Tyr Tyr Glu Met
77 65 70 75 80
78 Glu Ile Arg Pro Phe Ser His Gln Ile Tyr Pro Asp Leu Glu Pro Ala
79 85 90 95
80 Asn Met Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Ile Ile Val
81 100 105 110
82 Pro Arg Gly Thr Glu Ser Val Val Arg Phe Val Asn Ser Gly Glu Asn
83 115 120 125
84 Thr Ser Pro Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Pro
85 130 135 140
86 Phe Asp Gly Trp Ala Glu Asp Thr Thr Gln Pro Gly Glu Tyr Lys Asp
87 145 150 155 160
88 Tyr Tyr Tyr Pro Asn Arg Gln Ala Ala Arg Met Leu Trp Tyr His Asp
89 165 170 175
90 His Ala Met Ser Ile Thr Ala Glu Asn Ala Tyr Met Gly Gln Ala Gly
91 180 185 190
92 Val Tyr Met Ile Gln Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser
93 195 200 205
94 Gly Tyr Gly Glu Phe Asp Ile Pro Leu Val Leu Thr Ala Lys Arg Tyr
95 210 215 220
96 Asn Ala Asp Gly Thr Leu Phe Ser Thr Asn Gly Glu Val Ser Ser Phe
97 225 230 235 240
98 Trp Gly Asp Val Ile Gln Val Asn Gly Gln Pro Trp Pro Met Leu Asn
99 245 250 255
100 Val Gln Pro Arg Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser
101 260 265 270
102 Arg Ser Phe Ala Leu Tyr Leu Ala Thr Ser Glu Asp Ser Glu Thr Arg
103 275 280 285
104 Leu Pro Phe Gln Val Ile Ala Ala Asp Gly Gly Leu Leu Glu Gly Pro
105 290 295 300

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106 Val Asp Thr Asp Thr Leu Tyr Ile Ser Met Ala Glu Arg Trp Glu Val
107 305                               310                               315                               320
108 Val Ile Asp Phe Ser Thr Phe Ala Gly Gln Ser Ile Asp Ile Arg Asn
109                               325                               330                               335
110 Leu Pro Gly Ala Asp Gly Leu Gly Val Glu Pro Glu Phe Asp Asn Thr
111                               340                               345                               350
112 Asp Lys Val Met Arg Phe Val Val Asp Glu Val Leu Glu Ser Pro Asp
113                               355                               360                               365
114 Thr Ser Glu Val Pro Ala Asn Leu Arg Asp Val Pro Phe Pro Glu Gly
115                               370                               375                               380
116 Gly Asn Trp Asp Pro Ala Asn Pro Thr Asp Asp Glu Thr Phe Thr Phe
117 385                               390                               395                               400
118 Gly Arg Ala Asn Gly Gln Trp Thr Ile Asn Gly Val Thr Phe Ser Asp
119                               405                               410                               415
120 Val Glu Asn Arg Leu Leu Arg Asn Val Pro Arg Asp Thr Val Glu Ile
121                               420                               425                               430
122 Trp Arg Leu Glu Asn Asn Ser Asn Gly Trp Thr His Pro Val His Ile
123                               435                               440                               445
124 His Leu Val Asp Phe Arg Val Leu Ser Arg Ser Thr Ala Arg Gly Val
125                               450                               455                               460
126 Glu Pro Tyr Glu Ala Ala Gly Leu Lys Asp Val Val Trp Leu Ala Arg
127 465                               470                               475                               480
128 Arg Glu Val Val Tyr Val Glu Ala His Tyr Ala Pro Phe Pro Gly Val
129                               485                               490                               495
130 Tyr Met Leu His Cys His Asn Leu Ile His Glu Asp His Asp Met Met
131                               500                               505                               510
132 Ala Ala Phe Asn Val Thr Val Leu Gly Asp Tyr Gly Tyr Asn Tyr Thr
133                               515                               520                               525
134 Glu Phe Ile Asp Pro Met Glu Pro Leu Trp Arg Pro Arg Pro Phe Leu
135                               530                               535                               540
136 Leu Gly Glu Phe Glu Asn Gly Ser Gly Asp Phe Ser Glu Leu Ala Ile
137 545                               550                               555                               560
138 Thr Asp Arg Ile Gln Glu Met Ala Ser Phe Asn Pro Tyr Ala Gln Ala
139                               565                               570                               575
140 Asp Asp Asp Ala Ala Glu Glu
141                               580

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143 <210> SEQ ID NO: 3

144 <211> LENGTH: 2095

145 <212> TYPE: DNA

146 <213> ORGANISM: Stachybotrys chartarum

148 <400> SEQUENCE: 3

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150 atttcaaacg atcaacatga tcagccaagc tatcgagacc gtggctctgg gccttgctgt      120
151 gatcggcggc agctctgtcg atgccagatc cgttgctggt cgatcgacag acatgccttc      180
152 cggctctcacc aagaggcaga cgcagctgag tcctcccctg gccttgtagc aagtgcctct      240
153 gccgatccct cctctgaagg cgcccaagta gtaagtacat tctataggct agcagagcca      300
154 acgttgctaa tcattgcagt accgtcccca accccaacac tggagaggac atcttgtagt      360
155 acgagatgga gattaggccc ttctcccacc agatctaccc tgatctggag ccggccaaca      420
156 tggttggata cgatggcatg tccccaggac ctaccatcat cgttcctcgt ggcaactgaga      480

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158 gctctttctc tcgagctccc ttgatggtt gggctgagga cactaccag cctggcgagt 600
159 acaaggatta ctactacccc aacaggcagg ctgcccgcac gctttggtac catgaccatg 660
160 ccatgtccat caccgcccag aacgcctaca tgggtcaggc tgggtgtctac atgatccagg 720
161 acccggtcga ggatgccctg aacctcccca gcggtacgg cgagtttgat atcccccttg 780
162 ttctgactgc caagcgatac aacgcagacg gcaactctct ctccaccaat ggagagggtt 840
163 ccagcttctg gggtgacgtt attcaagtgg taagttgagc ccattgagat gcttcagatc 900
164 ctagaagtat cgatgtatga aattgtgcat gctctaacca gtgctatcac agaacggtca 960
165 gccttggcct atgctcaacg tgcagccgcg caagtaccgc ttccgcttcc tcaacgctgc 1020
166 cgtctcacgc tctttcgtc tgtatcttgc tacctctgag gattcagaga ccagacttcc 1080
167 cttccaggtc attgccgtg acggtgggtc gcttgagggc cctgttgaca ctgacactct 1140
168 gtacatctct atggccgagc gctggggagt tgttatcgac ttctccacct tcgctggcca 1200
169 gtccatcgat atccgcaacc ttctgggtgc tgacgggtctc ggtgttgagc ctgagtttga 1260
170 taacactgac aagggtcatgc gattcgctgt tgatgaagtc cttgagtcgc ccgacacttc 1320
171 tgaggtgcct gccaacctcc gagatgttcc tttccccgag ggcggcaact gggaccccg 1380
172 aaacccccact gatgacgaga ctttcacctt cggccgtgct aatggacagt ggacaatcaa 1440
173 cggagtacc ttctcggatg tcgagaaccg tctgctccgc aatgtgcccc gcgacactgt 1500
174 tgagatctgg cgacttgaga acaactcaa cggttgagc caccctgttc acattcacct 1560
175 cgttgacttc cgagtccttt ctcgttccac tgcccgtgga gtcgagcctt atgaggctgc 1620
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177 cgtcctttc ccgtaagttc tcgcctttta cctaactggt ttctactcat gctaacatct 1740
178 acaagtgggtg tctacatgtt gcactgccac aacctgatcc acgaggacca cgacatgatg 1800
179 gctgctttca atgtcactgt tctcggtgac tatggctaca actacaccga gttcattgac 1860
180 cccatggagc ctctctggag gccccgcccc ttctctctcg gagagttcga gaatggctcg 1920
181 ggtgacttca gcgagcttgc catcactgac cgcattcagg agatggctag cttcaacccc 1980
182 tacgcccagg ctgatgatga tgccgctgag gagtaaatat gatgatcgtc gaatgattta 2040
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185 <210> SEQ ID NO: 4

186 <211> LENGTH: 572

187 <212> TYPE: PRT

188 <213> ORGANISM: Myrothecium verucaria

190 <400> SEQUENCE: 4

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194 20 25 30
195 Gly His Leu Phe Lys Arg Val Ala Gln Ile Ser Pro Gln Tyr Pro Met
196 35 40 45
197 Phe Thr Val Pro Leu Pro Ile Pro Pro Val Lys Gln Pro Arg Leu Thr
198 50 55 60
199 Val Thr Asn Pro Val Asn Gly Gln Glu Ile Trp Tyr Tyr Glu Val Glu
200 65 70 75 80
201 Ile Lys Pro Phe Thr His Gln Val Tyr Pro Asp Leu Gly Ser Ala Asp
202 85 90 95
203 Leu Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Gln Val Pro
204 100 105 110
205 Arg Gly Val Glu Thr Val Val Arg Phe Ile Asn Asn Ala Glu Ala Pro
206 115 120 125
207 Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Ala Phe Asp Gly

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208      130      135      140
209 Trp Ala Glu Asp Ile Thr Glu Pro Gly Ser Phe Lys Asp Tyr Tyr Tyr
210 145      150      155      160
211 Pro Asn Arg Gln Ser Ala Arg Thr Leu Trp Tyr His Asp His Ala Met
212      165      170      175
213 His Ile Thr Ala Glu Asn Ala Tyr Arg Gly Gln Ala Gly Leu Tyr Met
214      180      185      190
215 Leu Thr Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser Gly Tyr Gly
216      195      200      205
217 Glu Phe Asp Ile Pro Met Ile Leu Thr Ser Lys Gln Tyr Thr Ala Asn
218      210      215      220
219 Gly Asn Leu Val Thr Thr Asn Gly Glu Leu Asn Ser Phe Trp Gly Asp
220 225      230      235      240
221 Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Lys Asn Val Glu Pro
222      245      250      255
223 Arg Lys Tyr Arg Phe Arg Phe Leu Asp Ala Ala Val Ser Arg Ser Phe
224      260      265      270
225 Gly Leu Tyr Phe Ala Asp Thr Asp Ala Ile Asp Thr Arg Leu Pro Phe
226      275      280      285
227 Lys Val Ile Ala Ser Asp Ser Gly Leu Leu Glu His Pro Ala Asp Thr
228      290      295      300
229 Ser Leu Leu Tyr Ile Ser Met Ala Glu Arg Tyr Glu Val Val Phe Asp
230 305      310      315      320
231 Phe Ser Asp Tyr Ala Gly Lys Thr Ile Glu Leu Arg Asn Leu Gly Gly
232      325      330      335
233 Ser Ile Gly Gly Ile Gly Thr Asp Thr Asp Tyr Asp Asn Thr Asp Lys
234      340      345      350
235 Val Met Arg Phe Val Val Ala Asp Asp Thr Thr Gln Pro Asp Thr Ser
236      355      360      365
237 Val Val Pro Ala Asn Leu Arg Asp Val Pro Phe Pro Ser Pro Thr Thr
238      370      375      380
239 Asn Thr Pro Arg Gln Phe Arg Phe Gly Arg Thr Gly Pro Thr Trp Thr
240 385      390      395      400
241 Ile Asn Gly Val Ala Phe Ala Asp Val Gln Asn Arg Leu Leu Ala Asn
242      405      410      415
243 Val Pro Val Gly Thr Val Glu Arg Trp Glu Leu Ile Asn Ala Gly Asn
244      420      425      430
245 Gly Trp Thr His Pro Ile His Ile His Leu Val Asp Phe Lys Val Ile
246      435      440      445
247 Ser Arg Thr Ser Gly Asn Asn Ala Arg Thr Val Met Pro Tyr Glu Ser
248      450      455      460
249 Gly Leu Lys Asp Val Val Trp Leu Gly Arg Arg Glu Thr Val Val Val
250 465      470      475      480
251 Glu Ala His Tyr Ala Pro Phe Pro Gly Val Tyr Met Phe His Cys His
252      485      490      495
253 Asn Leu Ile His Glu Asp His Asp Met Met Ala Ala Phe Asn Ala Thr
254      500      505      510
255 Val Leu Pro Asp Tyr Gly Tyr Asn Ala Thr Val Phe Val Asp Pro Met
256      515      520      525

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/19/2002
PATENT APPLICATION: US/09/656,640A TIME: 17:28:30

Input Set : A:\GC584-2-SEQLIST.TXT
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 12
Seq#:8; N Pos. 12,18